

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag		474
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln		
145	150	155
<210> 535		
<211> 158		
<212> PRT		
<213> Artificial		
<220>		
<223> modif. frag.; CFP F1DX, Y66W, N146I, and M153T mutations		
<400> 535		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1	5	10
		15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65	70	75
		80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 536

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, Y66W, N146I, and M153T mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 536

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag 471
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 537
 <211> 157
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1DX, Y66W, N146I, and M153T mutations,
 and posit. 1 Met removed

 <400> 537

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 538
 <211> 474
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1DX, with S65A mutation

<220>
 <221> CDS
 <222> (1)...(474)

<400> 538 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc gcc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgcc cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	474

<210>	539
<211>	158
<212>	PRT
<213>	Artificial

<220>
<223> modif. frag.; CFP F1DX, with S65A mutation

<400> 539

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 540

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, w. S65A mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 540

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

144

35

40

45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
 gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
145 150 155	
 <210> 541	
<211> 157	
<212> PRT	
<213> Artificial	
 <220>	
<223> modif. frag.; CFP F1DX, w. S65A mutation, and posit. 1 Met removed	
 <400> 541	
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
 Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 542

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations

<220>

<221> CDS

<222> (1)..(474)

<400> 542

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag		474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln		
145	150	155
<210> 543		
<211> 158		
<212> PRT		
<213> Artificial		
<220>		
<223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations		
<400> 543		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1	5	10
		15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65	70	75
		80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 544

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 544

gtg agc aag ggc qag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 545
 <211> 157
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations, and
 posit. 1 Met removed

 <400> 545

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

 <210> 546
 <211> 474
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; BFP F1DX, with Y66H mutation

<220>
 <221> CDS
 <222> (1)..(474)

<400> 546

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1			5						10						15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20						25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
				35			40							45			
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
				50			55							60			
ttc	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Phe	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
				65			70							80			
cg	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
				85				90						95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
				100				105						110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
				115			120							125			
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
				130			135							140			
aac	tac	aat	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag			474	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln				
				145			150							155			

<210> 547
<211> 158
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; BFP F1DX, with Y66H mutation

<400> 547

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 548

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, w. Y66H mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 548

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
 Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg	240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
145 150 155	
<210> 549	
<211> 157	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; BFP F1DX, w. Y66H mutation, and posit. 1 Met removed	
<400> 549	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 550

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations

<220>

<221> CDS

<222> (1)...(474)

<400> 550

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg . 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Gly Asn Tyr Lys Thr Arg Ala Glu

	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	145	150	155	474
 <210> 551				
<211> 158				
<212> PRT				
<213> Artificial				
 <220>				
<223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations				
 <400> 551				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60	
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140	

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 552
 <211> 471
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations, and
 posit. 1 Met removed

 <220>
 <221> CDS
 <222> (1)..(471)

 <400> 552

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1			5					10							15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag		96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
20								25							30		

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc		144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
35								40							45		

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctc		192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		
50								55							60		

ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg		240
Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
65								70							80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	qaa	ggc	tac	gtc	cag	gag	cgc		288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Gl	Gly	Tyr	Val	Gln	Glu	Arg		
								85							95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg		336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
								100							105		110

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc		384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
								115							120		125

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
								130							135		140

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag					471
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln					
								145							150		155

<220>
<223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations, and
posit. 1 Met removed

<400> 553

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 554
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations

<220>
<221> CDS
<222> (1)..(474)

<400>	554		48													
atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1	5								10						15	
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	96
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	144
			35			40							45			
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	192
			50			55							60			
ctc	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	
Leu	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	240
			65			70							75		80	
cgcg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	288
			85					90						95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	336
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	384
			115			120							125			
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	432
			130			135							140			
aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag			
Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln			474
			145			150							155			

<210> 555
<211> 158
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations

<400> 555

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10						15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 556

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations and posit.1
Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 556

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc		192	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
50	55	60	
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg		240	
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
130	135	140	
ttc aac agc cac aac gtc tat atc atg gcc gac aag cag		471	
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
145	150	155	
<210> 557			
<211> 157			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations and posit.1			
Met removed			
<400> 557			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
50	55	60	
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 558

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX with Y145F mutation

<220>

<221> CDS

<222> (1)..(474)

<400> 558

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			384
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			432
130	135	140	
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			474
145	150	155	
 <210> 559			
<211> 158			
<212> PRT			
<213> Artificial			
 <220>			
<223> modif. frag.; BFP F1DX with Y145F mutation			
 <400> 559			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 560

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX w. Y145F mutation and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 560

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag 471
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 561
 <211> 157
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; BFP F1DX w. Y145F mutation and posit. 1
 Met removed

 <400> 561

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 562
 <211> 474
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations

<220>
<221> CDS
<222> (1) .. (474)

<400> 562
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag 474
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 563
<211> 158
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations

<400> 563

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 564

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 564

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	144
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	192
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	240
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
ttc aac agc cac aac gtc tat atc atg gcc gac aag cag Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	471
145 150 155	
 <210> 565	
<211> 157	
<212> PRT	
<213> Artificial	
 <220>	
<223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations, and posit. 1 Met removed	
 <400> 565	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45	
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 566

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, with F46L mutation

<220>

<221> CDS

<222> (1)...(474)

<400> 566

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100	105	110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115	120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130	135	140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145	150	155	474
<210> 567			
<211> 158			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; Venus F1DX, with F46L mutation			
<400> 567			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50	55	60	
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115	120	125	

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 568

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, w. F46L mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 568

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac qtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 569
<211> 157
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1DX, w. F46L mutation, and posit. 1
Met removed

<400> 569

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 570
<211> 474
<212> DNA
<213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F46L, F64L mutations

 <220>
 <221> CDS
 <222> (1)..(474)

 <400> 570
 atg gtg agc aag ggc gag gac ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ctg ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cg_g cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgcc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag 474
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 571
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F46L, F64L mutations
 <400> 571

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1

5

10

15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 572

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, w. F46L, F64L mutations, and
 posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 572

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
145 150 155	

<210> 573

<211> 157

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, w. F46L, F64L mutations, and
posit. 1 Met removed

<400> 573

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
35 40 45	

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 574

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; SEYFP F1DX, w. F64L, M153T mutations

<220>

<221> CDS

<222> (1)..(474)

<400> 574

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg . 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc . 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc . 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc . 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag . 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag . 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag . 336
Arg Thr Ile Phe Phe Lys Asp Gly Asn Tyr Lys Thr Arg Ala Glu

	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				384
115	120		125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				432
130	135		140	
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln				474
145	150		155	
<210> 575				
<211> 158				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; SEYFP F1DX, w. F64L, M153T mutations				
<400> 575				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu				
1	5		10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20	25		30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35	40		45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				
50	55		60	
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys				
65	70		75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
85	90		95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
100	105		110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
115	120		125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
130	135		140	

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 576

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; SEYFP F1DX, F64L, M153T mutations, and
position 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 576

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag 471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 577
<211> 157
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; SEYFP F1DX, F64L, M153T mutations, and position 1 Met removed

<400> 577

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 578
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1DX, w. F64L, M153T mutations

<220>
<221> CDS
<222> (1) .. (474)

<210>	579
<211>	158
<212>	PRT
<213>	Artificial

<220>
<223> modif. frag.; Venus F1DX, w. F64L, M153T mutations

<400> 579

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10						15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 580

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, w. F64L, M153T mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)...(471)

<400> 580

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
50																60
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65																80
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
85																95
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
100																110
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
115																125
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
130																140
tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag				471
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln				
145																155
<210>	581															
<211>	157															
<212>	PRT															
<213>	Artificial															
<220>																
<223>	modif.	frag.	;	Venus	F1DX,	w.	F64L,	M153T	mutations,	and						
	posit.	1	Met	removed												
<400>	581															
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1																15
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
20																30
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
35																45
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
50																60
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65																80
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	

85

90

95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 582

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations

<220>

<221> CDS

<222> (1)..(474)

<400> 582

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1							5				10			15			

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
							20			25			30				

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile		
							35			40			45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
						50			55		60						

ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
						65			70		75		80				

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
							85			90			95				

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
							100			105			110				

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag 474
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

 <210> 583
 <211> 158
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations
 <400> 583

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 584

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations,
and position 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 584

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag 471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

<210> 585
 <211> 157
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations,
 and position 1 Met removed

 <400> 585

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

 <210> 586
 <211> 246
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFPF2DX, with Met added @ posit. 1

 <220>

<221> CDS
<222> (1)..(246)
<223> YFP F2DX corresponds to aa residues 159-239 of YFP

<400> 586
 atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

 gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30

 ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc tac cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45

 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

 tac aag 246
 Tyr Lys

<210> 587
 <211> 82
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; YFPF2DX, with Met added @ posit. 1

 <400> 587

 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30

 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45

 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

 Tyr Lys

<210> 588
 <211> 243
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFPF2DX, with Y203F mutation

 <220>
 <221> CDS
 <222> (1)..(243)

 <400> 588

aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
1 5 10 15	
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	
gac ggc ccc gtg ctg ctc gac aac cac tac ctg agc ttc cag tcc	144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser	
35 40 45	
gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
50 55 60	
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
65 70 75 80	
aag	243
Lys	

<210> 589
 <211> 81
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; YFPF2DX, with Y203F mutation

 <400> 589

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
1 5 10 15	
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser	
35 40 45	

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 590
<211> 246
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F2DX, w. Y203F mutation and Met added @ posit.
1

<220>
<221> CDS
<222> (1)..(246)

<400> 590
atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctc gac aac cac tac ctg agc ttc cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

~
ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag 246
Tyr Lys

<210> 591
<211> 82
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2DX, w. Y203F mutation and Met added @ posit.
1

<400> 591

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

Tyr Lys

<210> 592

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFPF2DX, with Y203H mutation

<220>

<221> CDS

<222> (1)..(243)

<400> 592

aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15 48

ggc agc gtg cag ctc gcc gac cac tac cag aac acc ccc atc ggc
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30 96

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc cac cag tcc
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
35 40 45 144

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60 192

gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg tac
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80 240

aag
Lys

243

<210> 593

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFPF2DX, with Y203H mutation

<400> 593

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 594

<211> 246

<212> DNA

<213> Artificial

<220>

<223> modif. frag.;YFP F2DX, w. Y203H mutation and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(246)

<400> 594

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

48

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

96

ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc cac cag		144	
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln			
35	40	45	
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg		192	
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu			
50	55	60	
ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg		240	
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu			
65	70	75	80
tac aag		246	
Tyr Lys			

<210> 595
<211> 82
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2DX, w. Y203H mutation and Met added @ posit. 1

<400> 595

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu			
1	5	10	15

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile		
20	25	30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln		
35	40	45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu		
50	55	60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu			
65	70	75	80

Tyr Lys

<210> 596
<211> 243
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F2DX, with Y203T mutation

<220>

<221> CDS
<222> (1)...(243)

<400> 596
aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc act cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

<210> 597

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, with Y203T mutation

<400> 597

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 598
 <211> 246
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F2DX, w. Y203T mutation and Met added @ posit.
 1

 <220>
 <221> CDS
 <222> (1)..(246)

 <400> 598

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
1 5 10 15	
 gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
20 25 30	
 ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc act cag	144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln	
35 40 45	
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
50 55 60	
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
65 70 75 80	
 tac aag	246
Tyr Lys	

<210> 599
 <211> 82
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F2DX, w. Y203T mutation and Met added @ posit.
 1

 <400> 599

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
1 5 10 15	
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
20 25 30	
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln	

35

40

45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

Tyr Lys

<210> 600

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations

<220>

<221> CDS

<222> (1)..(243)

<400> 600

aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac
 Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

48

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

96

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc acc cag tcc
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 35 40 45

144

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

192

gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg tac
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

240

aag

Lys

243

<210> 601

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations

<400> 601

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 602

<211> 246

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations and Met
added @ posit. 1

<220>

<221> CDS

<222> (1)..(246)

<400> 602

atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc agc gtg cag ctc gcc gac cac tac cag aac acc ccc atc 96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc acc cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag
Tyr Lys

246

<210> 603

<211> 82

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations and Met added @ posit. 1

<400> 603

Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

Tyr Lys

<210> 604

<211> 246

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2DX, with S175G mutation

<220>

<221> CDS

<222> (1)..(246)

<400> 604

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

48

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile

96

20

25

30

ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc tac cag	144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
35 40 45	
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
50 55 60	
ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg	240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
65 70 75 80	
tac aag	246
Tyr Lys	

<210> 605

<211> 82

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2DX, with S175G mutation

<400> 605

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
1 5 10 15	

Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
20 25 30	

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
35 40 45	

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
50 55 60	

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
65 70 75 80	

Tyr Lys

<210> 606

<211> 246

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2DX, w. S175G mutation and Met added @ posit. 1

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<220>
<221> CDS
<222> (1)..(246)

<400> 606
atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag
Tyr Lys 246

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<210> 607
<211> 82
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F2DX, w. S175G mutation and Met
      added @ posit. 1

<400> 607

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1           5                   10                  15

Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20          25                  30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
35          40                  45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50          55                  60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65          70                  75                  80

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Tyr Lys

<210> 608
<211> 243
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F2DX, w. V163A, S175G mutations

<220>
<221> CDS
<222> (1)...(243)

<400> 608
aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

<210> 609
<211> 81
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F2DX, w. V163A, S175G mutations

<400> 609
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 610

<211> 246

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2DX, w. V163A, S175G mutations and Met added @ posit. 1

<220>

<221> CDS

<222> (1)...(246)

<400> 610

atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc tac cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag
Tyr Lys

246

<210> 611

<211> 82

<212> PRT

<213> Artificial

<220>
<223> modif. frag.; Venus F2DX, w. V163A, S175G mutations and Met added @ posit. 1

<400> 611

Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

Tyr Lys

<210> 612
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F1D with position 1 Met removed

<220>
<221> CDS
<222> (1)..(474)
<223> YFP F1D corresponds to aa residues 1-159 of YFP

<400> 612
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 . 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

50	55	60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	65 70	75	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	85 90	95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	100 105	110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	115 120	125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	130 135	140	432
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	145 150	155	474
<210> 613			
<211> 158			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; YFP F1D with position 1 Met removed			
<400> 613			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe			
50	55	60	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90	95	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 614

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with K79R mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 614

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

115

120

125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140 432

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155 477

<210> 615
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D with K79R mutation

<400> 615

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 616
 <211> 474
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F1D w. K79R mutation, Met @ posit. 1 removed

 <220>
 <221> CDS
 <222> (1)..(474)

 <400> 616

gtg	agc	aag	ggc	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	tgc	acc	gtg	tcc	ggc	gag		96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
20								25						30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	tgc	atc	tgc		144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
35							40							45			

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc		192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
50							55						60				

ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg		240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
65						70					75				80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc		288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
85								90						95			

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg		336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
100							105				110						

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aat	cgc	atc	gag	ctg	aag	ggc	atc		384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
115							120						125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
130							135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag				474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys				
145							150				155						

<220>

<223> modif. frag.; YFP F1D w. K79R mutation, Met @ posit. 1 removed

<400> 617

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 618

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with Y66F mutation

<220>

<221> CDS

<222> (1)...(477)

<400> 618

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

48

1	5	10	15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc				96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20	25	30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc				144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35	40	45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc				192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				
50	55	60		
ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag				240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys				
65	70	75	80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
85	90	95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
100	105	110		
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
115	120	125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
130	135	140		
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag				477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys				
145	150	155		
<210> 619				
<211> 159				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; YFP F1D with Y66F mutation				
<400> 619				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu				
1	5	10	15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20	25	30		
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35	40	45		

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 620

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D w. Y66F mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 620

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg

240

65

70

75

80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85	90	95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100	105	110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115	120	125
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag		474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys		
145	150	155
<210> 621		
<211> 158		
<212> PRT		
<213> Artificial		
<220>		
<223> modif. frag.; YFP F1D w. Y66F mutation, Met @ posit. 1 removed		
<400> 621		
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1	5	10
		15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20	25	30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50	55	60
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65	70	75
		80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85	90	95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100	105	110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 622

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with Q69K mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 622

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130

135

140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

477

<210> 623
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F1D with Q69K mutation

<400> 623

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 624
<211> 474
<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D w. Q69K mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1) ..(474)

<400> 624

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 474
145 150 155

<210> 625

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1D w. Q69K mutation, Met @ posit. 1 removed

<400> 625

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 626

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1D w. V68L, Q69M mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 626

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 . 40 . 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 . 55 . 60	192
ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 . 70 . 75 . 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 . 90 . 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 . 105 . 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 . 120 . 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 . 135 . 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 . 150 . 155	477

<210> 627
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; citrine F1D w. V68L, Q69M mutations
<400> 627

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 . 5 . 10 . 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 . 25 . 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 . 40 . 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 . 55 . 60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 628

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1D w. V68L, Q69M mutations, Met @
posit.1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 628

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 629
 <211> 158
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; citrine F1D w. V68L, Q69M mutations, Met @
 posit.1 removed

 <400> 629

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 630

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with F64L mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 630

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130

135

140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

477

<210> 631
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with F64L mutation

<400> 631

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 632
<211> 474
<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with F64L mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 632

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 633

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with F64L mutation, Met @ posit. 1 removed

<400> 633

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 634

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with F46L mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 634

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

48

96

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 635

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with F46L mutation

<400> 635

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 636

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with F46L mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 636

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

	100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	115	120	125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	130	135	140	432
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	145	150	155	474
<210> 637				
<211> 158				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; YFP F1D with F46L mutation, Met @ posit. 1 removed				
<400> 637				
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15				
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30				
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45				
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60				
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80				
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95				
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110				
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125				
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140				

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 638

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with F46L, F64L mutations

<220>

<221> CDS

<222> (1)...(477)

<400> 638

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

192

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

240

cgc cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

336

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

384

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

432

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

477

<210> 639
 <211> 159
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F1D with F46L, F64L mutations

 <400> 639

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 640
 <211> 474
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F1D w. F46L, F64L mutations, and
 Met @ posit. 1 removed

<220>
 <221> CDS
 <222> (1)..(474)

<400> 640

gtg	agc	aag	ggc	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10				15				

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		96
20					25							30					

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	Cys		144
35					40					45							

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		192
50					55				60								

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg

Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		240
65					70				75			80					

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		288
85					90				95								

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg

Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		336
100					105					110							

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc

Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		384
115					120				125								

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac

Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		432
130					135				140								

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag

Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			474
145					150				155							

<210> 641
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D w. F46L, F64L mutations, and
 Met @ posit. 1 removed

<400> 641

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10				15				

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 642

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1D with F64L, M153T mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 642

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

144

35

40

45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

192

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

240

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

336

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

384

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

432

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

477

<210> 643
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1D with F64L, M153T mutations

<400> 643

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 644

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1D w. F64L, M153T mutations, and
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)...(474)

<400> 644

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 48
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 96
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 144
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 192
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 240
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 288
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 336

	100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile				384
115	120		125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn				432
130	135		140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys				474
145	150		155	
 <210> 645				
<211> 158				
<212> PRT				
<213> Artificial				
 <220>				
<223> modif. frag.; Venus F1D w. F64L, M153T mutations, and Met @ posit. 1 removed				
 <400> 645				
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15				
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30				
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45				
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60				
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80				
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95				
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110				
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125				
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140				

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys		
145	150	155
<210> 646		
<211> 477		
<212> DNA		
<213> Artificial		
<220>		
<223> modif. frag.; Venus F1D with F46L, M153T mutations		
<220>		
<221> CDS		
<222> (1)..(477)		
<400> 646		
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg		48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1 5 10 15		
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc		96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20 25 30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc		144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile		
35 40 45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc		192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50 55 60		
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag		240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65 70 75 80		
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag		288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85 90 95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag		336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100 105 110		
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115 120 125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130 135 140		
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag		477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys		
145 150 155		

<210> 647
 <211> 159
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1D with F46L, M153T mutations

 <400> 647

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 648
 <211> 474
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1D w. F46L, M153T mutations, and
 Met @ posit. 1 removed

<220>

<221> CDS

<222> (1) .. (474)

<400> 648

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

432

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

474

<210> 649

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1D w. F46L, M153T mutations, and
Met @ posit. 1 removed

<400> 649

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 650

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 650

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys 145 150 155	477
<210> 651	
<211> 159	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations	
<400> 651	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 652

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations,
Met @ position 1 removed

<220>

<221> CDS

<222> (1)...(474)

<400> 652

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys 145 150 155	474
<210> 653	
<211> 158	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations, Met @ position 1 removed	
<400> 653	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 654

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. F46L, F64L, N146I mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 654

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130

135

140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

477

<210> 655
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1D w. F46L, F64L, N146I mutations

<400> 655

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 656
<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F46L, F64L, N146I mutations,
Met @ position 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 656

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

432

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

474

<210> 657

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F46L, F64L, N146I mutations,

Met @ position 1 removed

<400> 657

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 658

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 658

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 659

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations

<400> 659

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 660

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations, and
Met @ position 1 removed

<220>

<221> CDS

<222> (1) .. (474)

<400> 660

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc			288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg			336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc			384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac			432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
130	135	140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag			474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys			
145	150	155	
<210> 661			
<211> 158			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations, and			
Met @ position 1 removed			
<400> 661			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
50	55	60	
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90	95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			

100

105

110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 662

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W mutation

<220>

<221> CDS

<222> (1)...(477)

<400> 662

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130

135

140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

477

<210> 663
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with Y66W mutation

<400> 663

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 664
<211> 474
<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 664

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 665

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W mutation, Met @ posit.. 1 removed

<400> 665

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 666

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W, N146I mutations

<220>

<221> CDS

<222> (1)...(477)

<400> 666

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cg ^g cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155	477
 <210> 667 <211> 159 <212> PRT <213> Artificial	
 <220> <223> modif. frag.; CFP F1D with Y66W, N146I mutations	
 <400> 667	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 668

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. Y66W, N146I mutations, and
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)...(474)

<400> 668

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15 48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30 96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45 144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60 192

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80 240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 669

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. Y66W, N146I mutations, and
Met @ posit. 1 removed

<400> 669

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 670

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W, M153T mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 670

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130

135

140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

477

<210> 671
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with Y66W, M153T mutations

<400> 671

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 672
<211> 474
<212> DNA

<213> Artificial
 <220>
 <223> modif. frag.; CFP F1D, w. Y66W and M153T mutations, and
 Met @ position 1 removed
 <220>
 <221> CDS
 <222> (1)..(474)

<400> 672

gtg	agc	aag	ggc	qag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5				10					15				

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		96
20					25				30								

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		144
35				40				45									

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		192
50				55				60									

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg

Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		240
65				70				75				80					

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		288
				85				90				95					

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg

Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		336
				100				105				110					

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc

Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		384
					115		120		125								

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac

Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		432
				130		135				140							

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag

Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys			474
145					150				155							

<210> 673
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D, w. Y66W and M153T mutations, and

Met @ position 1 removed

<400> 673

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 674

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with N146I mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 674

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc		96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc		144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc		192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag		240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65	70	75
80		
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag		288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85	90	95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag		336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag		477
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys		
145	150	155
<210> 675		
<211> 159		
<212> PRT		
<213> Artificial		
<220>		
<223> modif. frag.; CFP F1D with N146I mutation		
<400> 675		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1	5	10
15		
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 676

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. N146I mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1) ..(474)

<400> 676

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg

65	70	75	80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95				288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110				336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125				384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140				432
tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155				474
<210> 677				
<211> 158				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; CFP F1D w. N146I mutation, Met @ posit. 1 removed				
<400> 677				
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15				
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30				
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45				
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60				
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80				
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95				
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110				

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 678

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with M153T mutation

<220>

<221> CDS

<222> (1)...(477)

<400> 678

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

192

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

240

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

336

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

384

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
432

130

135

140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

477

<210> 679
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with M153T mutation

<400> 679

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 680
<211> 474
<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. M153T mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 680

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys 474
145 150 155

<210> 681

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. M153T mutation, Met @ posit. 1 removed

<400> 681

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 682

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with N146I, M153T mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 682

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 . 40 . 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 . 55 . 60	192
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 . 70 . 75 . 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 . 90 . 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 . 105 . 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 . 120 . 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 . 135 . 140	432
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys 145 . 150 . 155	477

<210> 683
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with N146I, M153T mutations
<400> 683

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 . 5 . 10 . 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 . 25 . 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 . 40 . 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 . 55 . 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 684

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. N146I, M153T mutations, and
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)...(474)

<400> 684

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag	474
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
145 150 155	

<210> 685

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. N146I, M153T mutations, and
Met @ posit. 1 removed

<400> 685

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 686

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. Y66W, N146I, and M153T mutations

<220>

<221> CDS

<222> (1)...(477)

<400> 686

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

192

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

240

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

336

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

384

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac

432

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag			477
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
145	150	155	
<210> 687			
<211> 159			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F1D, w. Y66W, N146I, and M153T mutations			
<400> 687			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
145	150	155	
<210> 688			
<211> 474			

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, Y66W, N146I, and M153T mutations,
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 688

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

432

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

474

<210> 689

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, Y66W, N146I, and M153T mutations,
Met @ posit. 1 removed

<400> 689

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 690

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with S65A mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 690

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

48

1	5	10	15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc				96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20	25	30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc				144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35	40	45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc				192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				
50	55	60		
ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag				240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys				
65	70	75	80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
85	90	95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
100	105	110		
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
115	120	125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
130	135	140		
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag				477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys				
145	150	155		
<210> 691				
<211> 159				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; CFP F1D with S65A mutation				
<400> 691				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu				
1	5	10	15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20	25	30		
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35	40	45		

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 692

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. S65A mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 692

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100	105	110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115	120	125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130	135	140	432
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145	150	155	474
<210> 693			
<211> 158			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F1D w. S65A mutation, Met @ posit. 1 removed			
<400> 693			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50	55	60	
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85	90	95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100	105	110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115	120	125	

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 694

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. S65A, Y66W, and S72A mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 694

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

477

<210> 695

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. S65A, Y66W, and S72A mutations

<400> 695

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 696

<211> 474

<212> DNA

<213> Artificial

<220>
<223> modif. frag.; CFP F1D, S65A, Y66W, and S72A mutations,
Met @ posit. 1 removed

<220>
<221> CDS
<222> (1)..(474)

<400> 696
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 697
<211> 158
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1D, S65A, Y66W, and S72A mutations,
Met @ posit. 1 removed

<400> 697

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 698

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D with Y66H mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 698

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
20 25 30.	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
50 55 60	
ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	477
145 150 155	
 <210> 699	
<211> 159	
<212> PRT	
<213> Artificial	
 <220>	
<223> modif. frag.; BFP F1D with Y66H mutation	
 <400> 699	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	

50

55

60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 700

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D w. Y66H mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1) .. (474)

<400> 700

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100	105	110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115	120	125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130	135	140	432
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145	150	155	474
<210> 701			
<211> 158			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1D w. Y66H mutation, Met @ posit. 1 removed			
<400> 701			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50	55	60	
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85	90	95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100	105	110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115	120	125	

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys		
145	150	155
<210> 702		
<211> 477		
<212> DNA		
<213> Artificial		
<220>		
<223> modif. frag.; BFP F1D w. F64L, Y66H mutations		
<220>		
<221> CDS		
<222> (1)..(477)		
<400> 702		
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg		48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1 5 10 15		
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc		96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20 25 30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc		144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35 40 45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc		192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50 55 60		
ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag		240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65 70 75 80		
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag		288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85 90 95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag		336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100 105 110		
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115 120 125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130 135 140		
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag		477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys		

145

150

155

<210> 703
<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; BFP F1D w. F64L, Y66H mutations
<400> 703

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 704
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; BFP F1D w. F64L, Y66H mutations, and

Met @ posit. 1 removed

<220>
<221> CDS
<222> (1)..(474)

<400> 704

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10				15				

gag

ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag		96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
20					25					30						

ggc

gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc		144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
35					40				45							

acc

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctc		192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		
50					55				60								

ggc

cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg		240
Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70				75				80			

cac

gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc		288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
85						90						95				

acc

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg		336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
100						105				110							

aag

ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc		384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
115						120				125						

gac

ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
130						135				140						

tac

aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag			474	
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			
145					150				155							

<210> 705
<211> 158
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; BFP F1D w. F64L, Y66H mutations, and Met @ posit. 1 removed

<400> 705

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

1

5

10

15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 706

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 706

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155	477
<210> 707	
<211> 159	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations	
<400> 707	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	

65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 708

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations,
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 708

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 709

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations,
Met @ posit. 1 removed

<400> 709

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 . . 120 . . 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 710

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, with Y145F mutation

<220>

<221> CDS

<222> (1) .. (477)

<400> 710

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 711

<211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1D, with Y145F mutation

<400> 711

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
	20					25				30					

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
	35					40				45					

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50				55					60					

Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
	65			70					75				80		

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
	85							90				95			

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
	100						105				110				

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
	115						120				125				

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130						135				140				

Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	
	145					150				155					

<210> 712
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1D, w. Y145F mutation, Met @ posit. 1 removed

<220>
 <221> CDS
 <222> (1)...(474)

<400> 712		
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc		48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag		96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20 25 30		
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc		144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35 40 45		
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc		192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50 55 60		
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg		240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65 70 75 80		
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cg		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85 90 95		
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gt		336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100 105 110		
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115 120 125		
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130 135 140		
ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag		474
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys		
145 150 155		

<210> 713

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. Y145F mutation, Met @ posit. 1 removed

<400> 713

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20 25 30		

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 714

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F46L, F64L, and Y145F mutations

<220>

<221> CDS

<222> (1)...(477)

<400> 714

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
50					55						60					
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70						75				80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85				90				95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
					100				105				110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
					115			120				125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
					130			135				140				
aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag		477
Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys		
					145			150				155				
<210>	715															
<211>	159															
<212>	PRT															
<213>	Artificial															
<220>																
<223>	modif.	frag.	;	BFP	F1D,	w.	F46L,	F64L,	and	Y145F	mutations					
<400>	715															
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10				15			
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
					20			25				30				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	
					35			40				45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
					50			55			60					
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
					65			70			75			80		
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85				90				95			

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 716

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F46L, F64L, and Y145F mutations,
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 716

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155	474
<210> 717	
<211> 158	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; BFP F1D, w. F46L, F64L, and Y145F mutations, Met @ posit. 1 removed	
<400> 717	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 718

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, w. Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(243)

<223> YFP F2D corresponds to aa residues 159-239 of YFP

<400> 718

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc qac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

<210> 719

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, w. Met added @ posit. 1

<400> 719

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly

20

25

30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

Lys

<210> 720

<211> 240

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, with Y203F mutation

<220>

<221> CDS

<222> (1)..(240)

<400> 720

aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15

48

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30

96

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45

144

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg gag
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

192

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

240

<210> 721

<211> 80

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, with Y203F mutation

<400> 721

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

<210> 722

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, w. Y203F mutation, Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(243)

<400> 722

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15 48

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30 96

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc tac cag tcc
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45 144

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60 192

gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg tac
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80 240

aag
Lys 243

<210> 723
<211> 81
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2D, w. Y203F mutation, Met added @ posit. 1

<400> 723

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 724
<211> 240
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F2D, with Y203H mutation

<220>
<221> CDS
<222> (1)..(240)

<400> 724
aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 48
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc gcc 144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala
35 40 45

ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag		192
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu		
50						55				60							
ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag		240
Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
65						70			75				80				
<210> 725																	
<211> 80																	
<212> PRT																	
<213> Artificial																	
<220>																	
<223> modif. frag.; YFP F2D, with Y203H mutation																	
<400> 725																	
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly																	
1			5			10			15								
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp																	
		20			25			30									
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala																	
		35			40			45									
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu																	
		50			55			60									
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys																	
		65			70			75			80						
<210> 726																	
<211> 243																	
<212> DNA																	
<213> Artificial																	
<220>																	
<223> modif. frag.; YFP F2D, w. Y203H mutation, Met added @ posit. 1																	
<220>																	
<221> CDS																	
<222> (1)..(243)																	
<400> 726																	
atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac																	
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp																	
1			5			10			15							48	
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc																	
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly																	
		20			25			30								96	

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc cac cag tcc	144		
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser			
35	40	45	
gcc ctg agc aaa gac ccc aac gag aag cgcc gat cac atg gtc ctg ctg	192		
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu			
50	55	60	
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240		
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr			
65	70	75	80
aag			243
Lys			

<210> 727
<211> 81
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2D, w. Y203H mutation, Met added @ posit. 1

<400> 727

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
1	5	10	15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		
20	25	30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser		
35	40	45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu		
50	55	60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr			
65	70	75	80

Lys

<210> 728
<211> 240
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F2D, with Y203T mutation

<220>
 <221> CDS
 <222> (1)..(240)

<400> 728 aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 1 5 10 15	48
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 20 25 30	96
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala 35 40 45	144
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 50 55 60	192
ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 65 70 75 80	240

<210> 729
 <211> 80
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2D, with Y203T mutation

<400> 729 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 1 5 10 15
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 20 25 30
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala 35 40 45
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 50 55 60
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 65 70 75 80

<210> 730
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2D, w. Y203T mutation, Met added @ posit. 1

 <220>
 <221> CDS
 <222> (1)..(243)

 <400> 730
 atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
 Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

 ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

 gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 144
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 35 40 45

 gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

 gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

 aag 243
 Lys

<210> 731
 <211> 81
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F2D, w. Y203T mutation, Met added @ posit. 1

 <400> 731

 Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 35 40 45

 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 732

<211> 240

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2D, w. V163A, Y203T mutations

<220>

<221> CDS

<222> (1)..(240)

<400> 732

aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

48

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

96

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
35 40 45

144

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

192

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

240

<210> 733

<211> 80

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2D, w. V163A, Y203T mutations

<400> 733

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

<210> 734

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag. CFP F2D, w. V163A, Y203T, Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(243)

<400> 734

atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 48
Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc acc cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

<210> 735

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag. CFP F2D, w. V163A, Y203T, Met added @ posit. 1

<400> 735

Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30.

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 736

<211> 240

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2D, with S175G mutation

<220>

<221> CDS

<222> (1)..(240)

<400> 736

aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

48

ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

96

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
35 40 45

144

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

192

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

240

<210> 737

<211> 80

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2D, with S175G mutation

<400> 737

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

<210> 738

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2D, w. S175G mutation, and Met added
@ posit. 1

<220>

<221> CDS

<222> (1)..(243)

<400> 738

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15 48

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30 96

gac ggc ccc gtg ctg ctc gac aac cac tac ctg agc tac cag tcc
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45 144

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60 192

gag ttc gtg acc gcc ggc ggg atc act ctc ggc atg gac gag ctg tac
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80 240

aag 243

Lys

<210> 739

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2D, w. S175G mutation, and Met added
@ posit. 1

<400> 739

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 740

<211> 240

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2D, w. V163A, S175G mutations

<220>

<221> CDS

<222> (1)..(240)

<400> 740

aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15 48

ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30 96

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45

 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

 ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

 <210> 741
 <211> 80
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F2D, w. V163A, S175G mutations
 <400> 741

 Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15

 Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30

 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45

 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

 <210> 742
 <211> 243
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag. Venus F2D, w. V163A, S175G, and Met added
 @ posit. 1

 <220>
 <221> CDS
 <222> (1)...(243)

 <400> 742
 atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac
 Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	
gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
35 40 45	
gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
50 55 60	
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
65 70 75 80	
aag	243
Lys	

<210> 743	
<211> 81	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag. Venus F2D, w. V163A, S175G, and Met added	
@ posit. 1	
<400> 743	
Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
1 5 10 15	
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
35 40 45	
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
50 55 60	
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
65 70 75 80	
Lys	

<210> 744	
<211> 519	
<212> DNA	

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<223> YFP F1E corresponds to aa residues 1-174 of YFP

<400> 744

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg^g
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

432

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

480

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

519

<210> 745

<211> 173

<212> PRT

<213> Artificial

<220>
<223> modif. frag.; YFP F1E, with position 1 Met removed

<400> 745

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 746

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with K79R mutation

<220>

<221> CDS

<222> (1)..(522)

<400> 746			
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg			48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1 5 10 15			
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc			96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20 25 30			
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35 40 45			
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50 55 60			
ttc ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg cgc			240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg			
65 70 75 80			
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85 90 95			
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100 105 110			
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115 120 125			
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130 135 140			
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145 150 155 160			
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac			522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
165 170			

<210> 747

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with K79R mutation

<400> 747

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1 5 10 15			

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 748

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with K79R mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 748

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

96

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
20								25						30	
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
35							40					45			
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe
50							55					60			
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	cgc	cgg
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg	Arg
65							70					75			80
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
85									90					95	
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
100								105					110		
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
115								120					125		
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
130								135					140		
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145												155			160
atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
165									170						

<210>	749
<211>	173
<212>	PRT
<213>	Artificial

<220>
<223> modif. frag.; YFP F1E, with K79R mutation, and posit. 1
Met removed

<400> 749

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35

40

45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 750

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with Y66F mutation

<220>

<221> CDS

<222> (1)...(522)

<400> 750

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1	5						10					15					

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
20						25						30					

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
35					40					45							

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	acc	ctc	gtg	acc	acc			192
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--	-----

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	522
165 170	
 <210> 751	
<211> 174	
<212> PRT	
<213> Artificial	
 <220>	
<223> modif. frag.; YFP F1E, with Y66F mutation	
 <400> 751	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 752

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with Y66F mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 752

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	519
165 170	
 <210> 753	
<211> 173	
<212> PRT	
<213> Artificial	
 <220>	
<223> modif. frag.; YFP F1E, with Y66F mutation, and posit. 1 Met removed	
 <400> 753	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	
 Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 754

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with Q69K mutation

<220>

<221> CDS

<222> (1)...(522)

<400> 754

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	384
	125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	432
	140		
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	145	150	480
	155	160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	165	170	522
<210> 755			
<211> 174			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; YFP F1E, with Q69K mutation			
<400> 755			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	1	5	10
			15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys	65	70	75
			80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 756

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with Q69K mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 756

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	
<210> 757	
<211> 173	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; YFP F1E, with Q69K mutation, and posit. 1 Met removed	
<400> 757	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

210 758

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations

<220>

<221> CDS

<222> (1) .. (522)

<400> 758

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atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
   1           5                   10                  15

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48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

192

ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag
 Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

240

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

336

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

384

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

432

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

480

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp

522

165

170

<210> 759
<211> 174
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations

<400> 759

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 760
<211> 519
<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations, and
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 760

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 761

<211> 173

<212> PRT

<213> Artificial

<220>
<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations, and
posit.1 Met removed

<400> 761

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 762
<211> 522
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, with F64L mutation

<220>

<221> CDS
<222> (1) .. (522)

<400> 762
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 763

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with F64L mutation

<400> 763

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30.

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 764

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 764

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

96

<210>	765
<211>	173
<212>	PRT
<213>	Artificial

<220>
<223> modif. frag.; CFP F1E, w. F64L mutation, and posit. 1
Met removed

<400> 765

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35

40

45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 766

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 766

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 767
<211> 174
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations

<400> 767

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 768

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 768
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	519
165 170	
 <210> 769	
<211> 173	
<212> PRT	
<213> Artificial	
 <220>	
<223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations, and	
posit. 1 Met removed	
 <400> 769	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	50 55 60
 Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 770

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 770

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac		480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn		
145	150	155
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac		522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
165	170	
<210> 771		
<211> 174		
<212> PRT		
<213> Artificial		
<220>		
<223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T, and V163A mutations		
<400> 771		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1	5	10
		15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65	70	75
		80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		

115

120

125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 772

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations, posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 772

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

115

120

125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 773

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations, posit. 1 Met removed

<400> 773

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 774

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with Y66W mutation

<220>

<221> CDS

<222> (1)...(522)

<400> 774

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn

145

150

155

160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170 522

<210> 775

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with Y66W mutation

<400> 775

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 776
 <211> 519
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1E, w. Y66W mutation, and posit. 1
 Met removed

 <220>
 <221> CDS
 <222> (1)...(519)

 <400> 776
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg 240
 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 777
 <211> 173
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1E, w. Y66W mutation, and posit. 1
 Met removed

 <400> 777

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 778
 <211> 522
 <212> DNA
 <213> Artificial

<220> modif. frag.; CFP F1E, with Y66W, N146I mutations
 <220>
 <221> CDS
 <222> (1)..(522)

 <400> 778
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<223> modif. frag.; CFP F1E, with Y66W, N146I mutations

<400> 779

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 780

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W; N146I mutations, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 780
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 781
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. Y66W, N146I mutations, and posit. 1
 Met removed

<400> 781

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 782

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with M153T mutation

<220>

<221> CDS

<222> (1)..(522)

<400> 782

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc

96

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
20						25					30					
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc															144	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
35						40					45					
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc															192	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
50						55					60					
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag															240	
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65						70					75				80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag															288	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
85						90					95					
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag															336	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
100						105					110					
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc															384	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
115						120					125					
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac															432	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
130						135					140					
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac															480	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
145						150					155				160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac															522	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
165						170										

<210> 783

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with M153T mutation

<400> 783

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1						5				10			15			

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
20						25					30					

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
35											40				45	

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 784

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. M153T mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 784

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	
<210> 785	
<211> 173	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; CFP F1E, w. M153T mutation, and posit. 1 Met removed	
<400> 785	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 786

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with N146I, M153T mutations

<220>

<221> CDS

<222> (1)...(522)

<400> 786

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20. 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys

65	70	75	80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85		90	95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100		105	110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115		120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130		135	140	432
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145		150	155	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165		170		522
<210> 787				
<211> 174				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; CFP F1E, with N146I, M153T mutations				
<400> 787				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1	5	10	15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20		25		30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35	40		45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50	55	60		
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65	70	75		80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85		90		95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 788

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. N146I, M153T mutations, and
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 788

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac aac tac aag acc cgc gcc gag gtg 336

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	519
165 170	

<210> 789

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. N146I, M153T mutations, and
posit.1 Met removed

<400> 789

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 790

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 790

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
130	135	140		
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac				480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn				
145	150	155	160	
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac				522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp				
165	170			
<210> 791				
<211> 174				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations				
<400> 791				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu				
1	5	10	15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20	25	30		
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35	40	45		
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				
50	55	60		
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys				
65	70	75	80	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
85	90	95		
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
100	105	110		
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
115	120	125		
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
130	135	140		
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn				
145	150	155	160	

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 792

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations; and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 792

```

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
   1           5           10          15

```

48

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
20								25						30	

96

```

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
      35          40          45

```

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc acc ttc
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

192

```

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80

```

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cg
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

288

```

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
          100           105           110

```

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130	135	140

432

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc
 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

480

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

519

<210> 793

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations, and
posit. 1 Met removed

<400> 793

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 794
 <211> 522
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations

 <220>
 <221> CDS
 <222> (1)..(522)

 <400> 794

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1																15	
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
																30	
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
																45	
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
																60	
ttc	ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Phe	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
																80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
																95	
cgc	acc	atc	ttc	ttc	aag	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag			336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
																110	
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
																125	
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
																140	
aac	tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn		
																160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
																170	

<210> 795

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations

<400> 795

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 796

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 796

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 797

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations,
and posit. 1 Met removed

<400> 797

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 798

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A mutations

<220>

<221> CDS

<222> (1) .. (522)

<400>	798																
atg	gtg	agc	aag	ggc	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10						15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	tgc	acc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
				20				25						30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	tgc	acc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
				35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
				50			55				60						
ttc	ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Phe	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
				65			70			75			80				
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
					85				90				95				
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
					100			105				110					
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
					115			120			125						
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
					130			135			140						
aac	tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn		
					145			150			155			160			
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				522
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
					165				170								

<210> 799

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A mutations

<400> 799

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1

5

10

15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 800

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A mutations, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 800

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gt	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aac ggc	480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 801

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A mutations, and posit. 1 Met removed

<400> 801

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 802

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with S65A mutation

<220>

<221> CDS

<222> (1)...(522)

<400> 802

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

144

35

40

45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
50 55 60	
ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	522
165 170	

<210> 803

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with S65A mutation

<400> 803

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 804

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 804

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240

Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	519
165 170	

<210> 805

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A mutation, and posit. 1
Met removed

<400> 805

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 806

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 806

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			384
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			432
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			480
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			522
165	170		
 <210> 807			
<211> 174			
<212> PRT			
<213> Artificial			
 <220>			
<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations			
 <400> 807			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 808

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 808

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	
<210> 809	
<211> 173	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations, and posit. 1 Met removed	
<400> 809	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 810

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A, Y66W, S72A, N146I, M153T,
and V163A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 810

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

<210> 812
 <211> 519
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1E, w. S65A, Y66W, S72A, N146I, M153T,
 and V163A mutations, position 1 Met removed

 <220>
 <221> CDS
 <222> (1)..(519)

<400> 812		
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc		48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag		96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20 25 30		
 ggc gaa ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc		144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35 40 45		
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc		192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50 55 60		
 gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg		240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65 70 75 80		
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
. 85 90 95		
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100 105 110		
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115 120 125		
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130 135 140		
 tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc		480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly		
145 150 155 160		
 atc aag gcc aac ttc aag atc cgc cac aac atc gag gac		519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
165 170		

<210> 813
<211> 173
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, w. S65A, Y66W, S72A, N146I, M153T,
and V163A mutations, position 1 Met removed

<400> 813

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 814
<211> 522
<212> DNA
<213> Artificial

<220>
 <223> modif. frag.; BFP F1E, with Y66H mutation

 <220>
 <221> CDS
 <222> (1)..(522)

 <400> 814

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48	
1 5 10 15		
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96	
20 25 30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144	
35 40 45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192	
50 55 60		
ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240	
65 70 75 80		
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288	
85 90 95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336	
100 105 110		
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384	
115 120 125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432	
130 135 140		
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480	
145 150 155 160		
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	522	
165 170		
<210> 815		
<211> 174		
<212> PRT		
<213> Artificial		
<220>		

<223> modif. frag.; BFP F1E, with Y66H mutation

<400> 815

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 816

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. Y66H mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 816		
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc		48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag		96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20 25 30		
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc		144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35 40 45		
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc		192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50 55 60		
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg		240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65 70 75 80		
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85 90 95		
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100 105 110		
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115 120 125		
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130 135 140		
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc		480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145 150 155 160		
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac		519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
165 170		

<210> 817
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1E, w. Y66H mutation, and posit. 1 Met removed
 <400> 817

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 818

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, with F64L, Y66H mutations

<220>

<221> CDS

<222> (1)...(522)

<400> 818

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35	40	45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50	55	60	192
ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65	70	75	240
cg ^g cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85	90	95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100	105	110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115	120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130	135	140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145	150	155	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165	170		522

<210> 819

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, with F64L, Y66H mutations

<400> 819

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 820

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H mutations, and
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 820

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc

192

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	cg	240	
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	Arg		
65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	cg	288	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	Arg		
85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	gt	336	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	Val		
100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	atc	384	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	Ile		
115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	aac	432	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	Asn		
130	135	140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	gg	480	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	Gly		
145	150	155	160
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac		519	
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
165	170		

<210> 821

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H mutations, and
posit.1 Met removed

<400> 821

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	Val		
1	5	10	15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	Glu		
20	25	30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	Cys		
35	40	45	

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	Leu		
50	55	60	

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	Arg		
65	70	75	80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 822

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 822

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac			522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
165	170		
<210> 823			
<211> 174			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations			
<400> 823			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 824

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 824

gtg agc aag ggc gag .gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

192

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 825
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations,
 and posit. 1 Met removed

<400> 825

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 826

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, with Y145F mutation

<220>

<221> CDS

<222> (1)..(522)

<400> 826

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130	135	140	
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160			480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170			522
<210> 827			
<211> 174			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1E, with Y145F mutation			
<400> 827			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15			
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30			
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45			
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60			
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80			
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95			
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110			
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125			
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140			
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160			

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 828

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. Y145F mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 828

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gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5                  10                 15

```

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

96

```

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
            35           40           45

```

144

192

```

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80

```

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cg
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

432

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

480

atc aag gtc aac ttc aag atc ccc cac aac atc gag gac

519

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 829

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. Y145F mutation, and posit. 1
Met removed

<400> 829

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 830

<211> 522
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1E, with F46L mutation

 <220>
 <221> CDS
 <222> (1)..(522)

 <400> 830

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 831
 <211> 174
 <212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F46L mutation

<400> 831

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 832

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L mutation, and posit. 1
Met removed

<220>
<221> CDS
<222> (1) .. (519)

<400> 832		
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc		48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag		96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20 25 30		
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc		144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys		
35 40 45		
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc		192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50 55 60		
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg		240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65 70 75 80		
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85 90 95		
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100 105 110		
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115 120 125		
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130 135 140		
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc		480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145 150 155 160		
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac		519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
165 170		

<210> 833

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L mutation, and posit. 1
Met removed

<400> 833

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 834

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F46L, F64L mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 834

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc

96

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile			
35	40	45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag			240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac			522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
165	170		
<210> 835			
<211> 174			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; Venus F1E, with F46L, F64L mutations			
<400> 835			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile			
35	40	45	

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 836

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, F64L mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 836

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg		192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
50	55	60
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg		240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65	70	75
80		
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85	90	95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100	105	110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115	120	125
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc		480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155
160		
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac		519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
165	170	

<210> 837

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, F64L mutations, and
posit. 1 Met removed

<400> 837

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1	5	10
		15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20	25	30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys		
35	40	45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
50	55	60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 838

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F46L, M153T mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 838

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

192

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys

240

65	70	75	80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95				288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110				336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125				384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140				432
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160				480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170				522
<210> 839				
<211> 174				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; Venus F1E, with F46L, M153T mutations				
<400> 839				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15				
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30				
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 40 45				
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60				
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80				
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95				

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 840

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 840

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg

336

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	519
165 170	

<210> 841

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T mutations, and
posit. 1 Met removed

<400> 841

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
35 40 45	

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 842

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F64L, M153T mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 842

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145	150	155	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165	170		522
<210> 843			
<211> 174			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; Venus F1E, with F64L, M153T mutations			
<400> 843			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50	55	60	
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130	135	140	
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145	150	155	160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 844

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w.F64L, M153T mutations, and
pos. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 844

```

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
   1           5           10          15

```

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

144

```

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc acc ctg
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
      50           55           60

```

192

```

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65           70           75           80

```

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

288

```

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
          100           105           110

```

336

```

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
           115          120          125

```

384

```

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130           135           140

```

432

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

480

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac

519

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 845

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w.F64L, M153T mutations, and
posit. 1 Met removed

<400> 845

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 846

<211> 522
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1E, w. F64L, M153T, and V163A mutations

 <220>
 <221> CDS
 <222> (1)..(522)

 <400> 846
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cg^g cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

 ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 522
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1E, w. F64L, M153T, and V163A mutations

 <400> 847

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

 <210> 848
 <211> 519
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1E, w.F64L, M153T, and V163A mutations,
 and posit. 1 Met removed

<220>
<221> CDS
<222> (1) .. (519)

<400> 848
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg^g 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 849

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w.F64L, M153T, and V163A mutations,
and posit. 1 Met removed

<400> 849

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 850

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 850

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	
<210> 851	
<211> 174	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations	
<400> 851	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 852

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 852

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	144
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	192
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	240
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	519
165 170	

<210> 853

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations,
and posit. 1 Met removed

<400> 853

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
35 40 45	

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 854

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, F64L, M153T, and
V163A mutations

<220>

<221> CDS

<222> (1)...(522)

<400> 854

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
50					55						60					
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70						75				80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90				95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
					100					105				110		
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
					115					120				125		
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
					130					135				140		
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
					145					150				155		
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
					165					170						
<210>	855															
<211>	174)
<212>	PRT															
<213>	Artificial															
<220>																
<223>	modif.	frag.	;	Venus	F1E,	w.	F46L,	F64L,	M153T,	and						
V163A	mutations															
<400>	855															
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1					5						10				15	
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
					20						25				30	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	
					35						40				45	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
50						55						60				
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	

65

70

75

80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155					160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 856
<211> 519
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, w. F46L, F64L, M153T, and V163A mutations, and posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(519)

<400> 856
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

```

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
          35           40           45

```

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc acc ctg
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg

65

70

75

80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 857
<211> 173
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, w. F46L, F64L, M153T, and V163A mutations, and posit. 1 Met removed

<400> 857

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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1           5           10          15

```

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 858

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with V163A mutation

<220>

<221> CDS

<222> (1)..(522)

<400> 858

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

192

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

240

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
Arg Thr Ile Phe Phe Lys Asp Gly Asn Tyr Lys Thr Arg Ala Glu

336

	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				384
115	120		125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				432
130	135		140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn				480
145	150		155	
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp				522
165	170			
 <210> 859				
<211> 174				
<212> PRT				
<213> Artificial				
 <220>				
<223> modif. frag.; Venus F1E, with V163A mutation				
 <400> 859				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu				
1	5		10	
				15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20		25		30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35		40		45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				
50		55		60
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys				
65		70		75
				80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
85		90		95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
100		105		110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
115		120		125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 860

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. V163A mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)...(519)

<400> 860

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	
<210> 861	
<211> 173	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; Venus F1E, w. V163A mutation, and posit. 1 Met removed	
<400> 861	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 862
 <211> 522
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1E, with M153T, V163A mutations

 <220>
 <221> CDS
 <222> (1)..(522)

 <400> 862

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10						15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
20						25								30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
35						40								45			
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50						55								60			
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65						70								80			
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
85									90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
100									105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
115						120								125			
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
130								135						140			
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn		
145									150				155		160		
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				522
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				

165

170

<210> 863

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with M153T, V163A mutations

<400> 863

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 864

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. M153T, V163A mutations, and
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 864

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 865

<211> 173

<212> PRT

<213> Artificial

<220>
<223> modif. frag.; Venus F1E, w. M153T, V163A mutations, and
posit.1 Met removed

<400> 865

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 866

<211> 198

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2E, with Met added @ position 1

<220>

<221> CDS
<222> (1)..(198)
<223> YFP F2E corresponds to aa residues 175-end of YFP

<400> 866

atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc tac cag 96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
20 25 30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

tac aag 198
Tyr Lys
65

<210> 867

<211> 66

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2E, with Met added @ position 1

<400> 867

Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

Tyr Lys
65

<210> 868

<211> 195

<212> DNA

<210> 870
 <211> 198
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2E, w. Y203F mutation, Met added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(198)

<400> 870

atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	48
Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
1 5 10 15	
ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc ttc cag	96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln	
20 25 30	
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
35 40 45	
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
50 55 60	
tac aag	198
Tyr Lys	
65	

<210> 871
 <211> 66
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2E, w. Y203F mutation, Met added @ posit. 1

<400> 871

Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	1
	5 10 15
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln	20 25 30
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	35 40 45
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	50 55 60

Tyr Lys
65

<210> 872
<211> 195
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F2E, with Y203H mutation

<220>
<221> CDS
<222> (1)..(195)

<400> 872
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 48
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc 96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
20 25 30

gcc ctg agc aaa gac ccc aac gag aag cgcc gat cac atg gtc ctg ctg 144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

aag 195
Lys
65

<210> 873
<211> 65
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2E, with Y203H mutation

<400> 873

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
20 25 30

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

Lys
65

<210> 874

<211> 198

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2E, w. Y203H mutation, Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(198)

<400> 874

atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag 96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
20 25 30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg 192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

tac aag

198

Tyr Lys

65

<210> 875

<211> 66

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2E, w. Y203H mutation, Met added @ posit. 1

<400> 875

Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

Tyr Lys
65

<210> 876

<211> 195

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2E, with S175G mutation

<220>

<221> CDS

<222> (1)..(195)

<400> 876

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15

48

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc tac cag tcc
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
20 25 30

96

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

144

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

192

aag

195

Lys

65

<210> 877

<211> 65

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2E, with S175G mutation

<400> 877

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
20 25 30

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

Lys
65

<210> 878

<211> 198

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2E, w. S175G mutation , Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(198)

<400> 878

atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
20 25 30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg 192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

tac aag

Tyr Lys

65

198

<210> 879

<211> 66

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2E, w. S175G mutation , Met added @ posit. 1

<400> 879

Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

Tyr Lys
65

<210> 880

<211> 195

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2E, w. S175G, Y203T mutations

<220>

<221> CDS

<222> (1)..(195)

<400> 880

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15

48

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
20 25 30

96

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

144

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

192

aag

195

Lys

65

<210> 881

<211> 65

<212> PRT

<213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203T mutations
 <400> 881

Gly	Gly	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly
1				5					10					15	

Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser
									25					30	

Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu
									40				45		

Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr
									55				60		

Lys

65

<210> 882
 <211> 198
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203T mutations, and
 Met added @ position 1

<220>
 <221> CDS
 <222> (1)...(198)

<400>	882														
atg	ggc	ggc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc
Met	Gly	Gly	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile
1				5						10				15	

ggc	gac	ggc	ccc	gtg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	
Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln
										25			30		

tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg
Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Ile
										45					

ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg
Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu
									55			60			

tac	aag														
Tyr	Lys														

<210> 883
<211> 66
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G, Y203T mutations, and
Met added @ position 1

<400> 883

Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

Tyr Lys
65

<210> 884
<211> 195
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G, Y203F mutations

<220>
<221> CDS
<222> (1)..(195)

<400> 884
ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 48
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15

gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc ttc cag tcc 96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
20 25 30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

aag 195
Lys
65

<210> 885
<211> 65
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G, Y203F mutations

<400> 885

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
5 10 15

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
20 25 30

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

Lys
65

<210> 886
<211> 198
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G, Y203F mutations, and
Met added @ position 1

<220>
<221> CDS
<222> (1)..(198)

<400> 886
atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc acc ccc atc 48
Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

ggc gac ggc ccc gtg ctg ccc gac aac cac tac ctg agc ttc cag 96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
20 25 30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
35 40 45	
ctg gag ttc gtg acc gcc ggg atc act ctc ggc atg gac gag ctg	192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
50 55 60	
tac aag	198
Tyr Lys	
65	

<210> 887
<211> 66
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G, Y203F mutations, and Met added @ position 1

<400> 887

Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

Tyr Lys
65

<210> 888
<211> 570
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F1F, with position 1 Met removed

<220>
<221> CDS
<222> (1)..(570)
<223> YFP F1F corresponds to aa residues 1-191 of YFP

<400> 888
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc		192	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe			
50	55	60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg		240	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
130	135	140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc		480	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
145	150	155	160
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg		528	
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
165	170	175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac		570	
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180	185	190	

<210> 889

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with position 1 Met removed

<400> 889

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1	5	10	15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20	25	30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35	40	45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 890

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with K79R mutation

<220>

<221> CDS

<222> (1)...(573)

<400> 890

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

144

35

40

45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

<210> 891

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with K79R mutation

<400> 891

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15
--

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 892

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. K79R mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 892

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	144
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	192
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	240
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	528
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	570
180 185 190	
 <210> 893	
<211> 190	
<212> PRT	
<213> Artificial	
 <220>	
<223> modif. frag.; YFP F1F, w. K79R mutation, and posit. 1 Met removed	
 <400> 893	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 894

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with Y66F mutation

<220>

<221> CDS

<222> (1)..(573)

<400> 894

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

48

96

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

<210> 895

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with Y66F mutation

<400> 895

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15
--

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 896

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. Y66F mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 896

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

96

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

ggc ttc ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag cg 240
 Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cg 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gt 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgcc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgcc cac aac atc gag gac ggc agc gt 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 897
 <211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1F, w. Y66F mutation, and posit. 1
 Met removed

<400> 897

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 898

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with Q69K mutation

<220>

<221> CDS

<222> (1)..(573)

<400> 898

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35	40	45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50	55	60	192
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65	70	75	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85	90	95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100	105	110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115	120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130	135	140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145	150	155	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165	170	175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180	185	190	573
<p><210> 899 <211> 191 <212> PRT <213> Artificial</p> <p><220> <223> modif. frag.; YFP F1F, with Q69K mutation</p> <p><400> 899</p> <p>Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15</p> <p>Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30</p>			

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 900

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. Q69K mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 900

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

48

96

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
 Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 901

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. .frag.; YFP F1F, w. Q69K mutation, and posit. 1
Met removed

<400> 901

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 . 10 . 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 902

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1F, w. V68L, Q69M mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 902

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35	40	45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50	55	60	192
ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65	70	75	240
cg ^g cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85	90	95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100	105	110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115	120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130	135	140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145	150	155	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165	170	175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180	185	190	573

<210> 903

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; citrine F1F, w. V68L, Q69M mutations

<400> 903

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 904

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1F, w. V68L, Q69M mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 904

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

96

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	144
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	192
50 55 60	
ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	240
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	480
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	528
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	570
180 185 190	
<210> 905	
<211> 190	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; citrine F1F, w. V68L, Q69M mutations, and posit. 1 Met removed	
<400> 905	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 906

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with F64L mutation

<220>

<221> CDS

<222> (1)..(573)

<400> 906

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35	40	45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50	55	60	192
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65	70	75	240
cg ^g cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85	90	95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100	105	110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115	120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130	135	140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145	150	155	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165	170	175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180	185	190	573
<p><210> 907 <211> 191 <212> PRT <213> Artificial</p> <p><220> <223> modif. frag.; CFP F1F, with F64L mutation</p> <p><400> 907</p> <p>Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15</p> <p>Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30</p>			

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Glu Asp
180 185 190

<210> 908

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L mutation, posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 908

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

96

20

25

30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 909
 <211> 190
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1F, w. F64L mutation, posit. 1 Met removed

 <400> 909

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 910

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 910

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

96

	20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				144
35	40		45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				192
50	55		60	
ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys				240
65	70		75	80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				288
85	90			95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				336
100	105		110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				384
115	120		125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				432
130	135		140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn				480
145	150		155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser				528
165	170		175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp				573
180	185		190	
<210> 911				
<211> 191				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations				
<400> 911				
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu				
1	5		10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20	25		30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 912

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 912

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg	240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	
<210> 913	
<211> 190	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations, and posit. 1 Met removed	
<400> 913	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 914

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 914			
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg			48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1 5 10 15			
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc			96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20 25 30			
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35 40 45			
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50 55 60			
ctg acc tgg ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag			240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65 70 75 80			
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85 90 95			
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100 105 110			
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115 120 125			
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130 135 140			
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac			480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn			
145 150 155 160			
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165 170 175			
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180 185 190			

<210> 915
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
 and V163A mutations

<400> 915

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 916

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations, and position 1 Met removed

<220>

<221> CDS
<222> (1)..(570)

<400> 916
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tat atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 917
<211> 190
<212> PRT
<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations, and position 1 Met removed

<400> 917

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 918

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with Y66W mutation

<220>
 <221> CDS
 <222> (1)...(573)

<400> 918

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10						15		

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		96
20							25							30			

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		144
35							40						45				

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Va	Thr	Thr		192
50							55					60					

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag

Phe	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		240
65							70					75		80			

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		288
85							90					95					

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		336
100							105					110					

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		384
115							120					125					

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		432
130							135					140					

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		480
145							150					155		160			

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc

Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		528
165							170					175					

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		573	
180							185					190					

<210> 919
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, with Y66W mutation
 <400> 919

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
	20						25						30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
	35					40						45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Phe	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
	65				70				75				80		

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
	85					90							95		

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
	100						105					110			

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
	115					120						125			

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
	145					150				155			160		

Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
	165						170					175			

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
	180						185					190			

<210> 920
 <211> 570
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. Y66W mutation, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 920 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc tgg ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570
<210> 921 <211> 190 <212> PRT <213> Artificial	

<220>
<223> modif. frag.; CFP F1F, w. Y66W mutation, and posit. 1 Met removed
<400> 921

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 922
<211> 573
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations

<220>
<221> CDS
<222> (1) .. (573)

<400> 922			
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg			48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1 5 10 15			
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc			96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20 25 30			
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35 40 45			
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50 55 60			
ttc ggc tgg ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag			240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65 70 75 80			
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85 90 95			
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100 105 110			
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115 120 125			
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130 135 140			
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145 150 155 160			
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165 170 175			
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180 185 190			
<210> 923			
<211> 191			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations			
<400> 923			

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 924

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 924

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgcc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgcc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgcc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgcc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 925

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations, and
posit. 1 Met removed

<400> 925

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 926

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with M153T mutation

<220>

<221> CDS
<222> (1)..(573)

<400> 926		
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg		48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1 5 10 15		
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc		96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20 25 30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc		144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35 40 45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc		192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50 55 60		
ttc ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag		240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65 70 75 80		
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag		288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85 90 95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag		336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100 105 110		
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115 120 125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130 135 140		
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac		480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn		
145 150 155 160		
ggc atc aag gtg aac ttc aag atc cgcc cac aac atc gag gac ggc agc		528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
165 170 175		
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac		573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp		
180 185 190		

<210> 927
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, with M153T mutation

<400> 927

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 928

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. M153T mutation, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 928

gtg	agc	aag	ggc	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10				15				

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		96
									20			25			30		

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		144
								35			40		45				

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		192
						50			55			60					

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg

Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		240
					65		70		75			80					

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		288
						85			90			95					

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg

Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		336
						100			105			110					

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc

Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		384
						115			120			125					

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac

Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		432
						130		135			140						

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc

Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly		480
						145			150			155		160			

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg

Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		528
						165			170			175					

gag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac

Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			570
							180			185		190				

<210> 929
 <211> 190
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. M153T mutation, and posit. 1 Met removed

<400> 929

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 930

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with M153T mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 930		
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
1 5 10 15		
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20 25 30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35 40 45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50 55 60		
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240	
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65 70 75 80		
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85 90 95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100 105 110		
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115 120 125		
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130 135 140		
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480	
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn		
145 150 155 160		
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528	
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
165 170 175		
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573	
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp		
180 185 190		

<210> 931
 <211> 191
 <212> PRT
 <213> Artificial

<220>
<223> modif. frag.; CFP F1F, with M153T mutation

<400> 931

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 932
<211> 570
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. N146I, M153T mutations, and

posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(570)

<400> 932
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 933
<211> 190
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. N146I, M153T mutations, and
posit. 1 Met removed

<400> 933

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 934
<211> 573
<212> DNA
<213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations

 <220>
 <221> CDS
 <222> (1)..(573)

 <400> 934

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160	480
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573
<210> 935 <211> 191 <212> PRT	

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations

<400> 935

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 936

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 936
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tat atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 937

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations,

and posit. 1 Met removed

<400> 937

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 938

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 938
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgcc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 939
<211> 191
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations

<400> 93.9

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 940

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations,

and posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(570)

<400>	940																
gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5				10					15				
gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag		96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
		20						25					30				
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc		144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
		35						40					45				
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc		192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
		50						55					60				
ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg		240
Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
		65						70					75		80		
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc		288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
								85					90		95		
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg		336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
								100					105		110		
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc		384
Lys	Phe	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile			
								115					120		125		
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
								130					135		140		
tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	ggc		480
Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
								145					150		155		160
atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg		528
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
								165					170		175		
cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac				570
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp				
								180					185		190		

<210> 941
<211> 190
<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations,
and posit. 1 Met removed

<400> 941

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 942

<211> 573

<212> DNA

<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 942
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 943
<211> 191
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations

<400> 943

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 944

<211> 570
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations, and posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(570)

<400> 944
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15 48
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30 96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45 144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60 192
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80 240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95 288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110 336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125 384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140 432
tat atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160 480
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175 528
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 570

180

185

190

<210> 945

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations, and posit. 1 Met removed

<400> 945

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 946
 <211> 573
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1F, with S65A mutation

 <220>
 <221> CDS
 <222> (1)...(573)

 <400> 946

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1																15	
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
20																30	
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
35																45	
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50																60	
ttc	gcc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Phe	Ala	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65																80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
85																95	
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
100																110	
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
115																125	
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
130																140	
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145																160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc		528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
165																175	
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			573

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 947

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with S65A mutation

<400> 947

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 949
 <211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. S65A mutation, and posit. 1
 Met removed

<400> 949

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1					5					10				15	

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 950

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. S65A, Y66W, and S72A mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 950

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

165

170

175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190 573

<210> 951
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. S65A, Y66W, and S72A mutations

<400> 951

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 952

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. S65A, Y66W, and S72A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 952

qtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag cgg 240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 954

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. S65A, Y66W, S72A, N146I, M153T,
and V163A mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 954

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aac 480

Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gcc	aac	tcc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170					175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
					180			185				190				
<210>	955															
<211>	191															
<212>	PRT															
<213>	Artificial															
<220>																
<223>	modif.	frag.	;	CFP	F1F,	w.	S65A,	Y66W,	S72A,	N146I,	M153T,					
and	V163A	mutations														
<400>	955															
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1					5					10				15		
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
						20			25				30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
					35			40				45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
					50			55			60					
Phe	Ala	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
					65			70.		75			80			
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85				90				95			
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
					100			105				110				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
					115			120			125					
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
					130			135			140					
Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	

145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 956

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. S65A, Y66W, S72A, N146I, M153T,
and V163A mutations, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 956

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn

130	135	140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145	150	155	480
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165	170	175	528
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180	185	190	570
<210> 957			
<211> 190			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F1F, w. S65A, Y66W, S72A, N146I, M153T, and V163A mutations, and posit. 1 Met removed			
<400> 957			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15			
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30			
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45			
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60			
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80			
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95			
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110			
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125			
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140			

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 958

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, with Y66H mutation

<220>

<221> CDS

<222> (1)..(573)

<400> 958

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180	185	190	
<210> 959			
<211> 191			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1F, with Y66H mutation			
<400> 959			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 960

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. Y66H mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 960

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
130	135	140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc			480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
145	150	155	160
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg			528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
165	170	175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180	185	190	
<210> 961			
<211> 190			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1F, w. Y66H mutation, and posit. 1 Met removed			
<400> 961			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe			
50	55	60	
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90	95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100	105	110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
115	120	125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
130	135	140	

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 962

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H mutations

<220>

<221> CDS

<222> (1)...(573)

<400> 962

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180	185	190	
<210> 963			
<211> 191			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1F, w. F64L, Y66H mutations			
<400> 963			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 964

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 964		
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc		48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag		96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20 25 30		
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc		144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35 40 45		
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg		192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
50 55 60		
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cg		240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65 70 75 80		
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85 90 95		
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg		336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100 105 110		
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc		384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115 120 125		
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac		432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130 135 140		
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc		480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145 150 155 160		
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg		528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
165 170 175		
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac		570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp		
180 185 190		

<210> 965

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H mutations, and
posit. 1 Met removed

<400> 965

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 966

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 966			
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg			48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1 5 10 15			
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc			96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20 25 30			
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35 40 45			
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50 55 60			
ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag			240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65 70 75 80			
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85 90 95			
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100 105 110			
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115 120 125			
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130 135 140			
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145 150 155 160			
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165 170 175			
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180 185 190			

<210> 967

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations

<400> 967

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 968

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations,
and posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(570)

<400> 968
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 969
<211> 190
<212> PRT
<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations,
and posit. 1 Met removed

<400> 969

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 970

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, with Y145F mutation

<220>

<221> CDS

<222> (1)..(573)

<400> 970

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

192

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

240

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

336

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

384

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

432

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

480

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

528

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

573

<210> 971

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, with Y145F mutation

<400> 971

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 972

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. Y145F mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)...(570)

<400> 972

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

432

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

480

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

528

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

570

<210> 973

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. Y145F mutation, and posit. 1 Met removed

<400> 973

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 974

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 974
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 975
<211> 191
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations
<400> 975

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 976
<211> 570
<212> DNA
<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 976

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 977

<211> 190
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations,
and posit. 1 Met removed

<400> 977

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 978
<211> 573

<212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1F, with V163A mutation

 <220>
 <221> CDS
 <222> (1)..(573)

 <400> 978

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

<210> 979
<211> 191
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, with V163A mutation

<400> 979

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 980
<211> 570

<212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1F, w. V163A mutation, posit. 1 Met removed

 <220>
 <221> CDS
 <222> (1)..(570)

 <400> 980

gtg	agc	aag	ggc	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10						15		
gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	tgc	acc	gtg	tcc	ggc	gag		96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
					20				25					30			
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	tgc	atc	tgc		144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
					35			40				45					
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc		192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
					50			55				60					
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg		240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
					65			70				75			80		
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc		288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
					85			90				95					
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg		336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
					100			105				110					
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc		384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
					115			120				125					
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
					130			135				140					
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc		480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
					145			150				155			160		
atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg		528
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
					165			170				175					
cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac				570
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp				
					180			185				190					

<210> 981
 <211> 190
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1F, w. V163A mutation, posit. 1 Met removed

 <400> 981

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 982
 <211> 573

<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. M153T, V163A mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 982			
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg			48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1 5 10 15			
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc			96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20 25 30			
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35 40 45			
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50 55 60			
ttc ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag			240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65 70 75 80			
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85 90 95			
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100 105 110			
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115 120 125			
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130 135 140			
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn			
145 150 155 160			
ggc atc aag gcc aac ttc aag atc cgcc cac aac atc gag gac ggc agc			528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165 170 175			
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180 185 190			

<210> 983
<211> 191<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. M153T, V163A mutations

<400> 983

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 984

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A mutations, and
posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 984 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570
<210> 985 <211> 190 <212> PRT <213> Artificial	
<220>	

<223> modif. frag.; Venus F1F, w. M153T, V163A mutations, and
posit. 1 Met removed

<400> 985

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 986

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, with S175G mutation

<220>
 <221> CDS
 <222> (1)...(573)

<400> 986

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
ttc ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgcc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
ggc atc aag gtg aac ttc aag atc cgcc cac aac atc gag gac ggc ggc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly 165 170 175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573
<210> 987 <211> 191 <212> PRT <213> Artificial	

<220>
<223> modif. frag.; Venus F1F, with S175G mutation

<400> 987

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 988

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. S175G mutation, posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 988

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10					15			

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		96
20					25							30					

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		144
35					40					45							

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		192
50					55					60							

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg

Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		240
65					70				75				80				

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		288
85							90					95					

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg

Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		336
100							105				110						

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc

Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		384
115						120				125							

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac

Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		432
130						135				140							

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc

Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		480
145						150			155			160					

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg

Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val		528
165							170				175						

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac

Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			570	
180							185				190						

<210> 989
 <211> 190
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. S175G mutation, posit. 1 Met removed

<400> 989

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 990

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, S175G mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 990			
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg			48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1 5 10 15			
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc			96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20 25 30			
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35 40 45			
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50 55 60			
ttc ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag			240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65 70 75 80			
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85 90 95			
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100 105 110			
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115 120 125			
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130 135 140			
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn			
145 150 155 160			
ggc atc aag gtg aac ttc aag atc cgcc cac aac atc gag gac ggc ggc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly			
165 170 175			
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
180 185 190			

<210> 991
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. M153T, S175G mutations

<400> 991

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 992

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, S175G mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 992

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

96

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

144

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

192

ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag cgg
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

240

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

288

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

336

aag ttc gag ggc gac acc ctg gtg aac cgcc atc gag ctg aag ggc atc
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

384

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

432

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

480

atc aag gtg aac ttc aag atc cgcc cac aac atc gag gac ggc ggc gtg
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

528

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

570

<210> 993

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, S175G mutations, and
posit. 1 Met removed

<400> 993

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 994

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. V163A, S175G mutations

<220>

<221> CDS
 <222> (1)..(573)

<400> 994

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10						15		

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		96
20							25							30			

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		144
35							40						45				

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		192
50							55					60					

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag

Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		240
65							70					75		80			

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		288
85							90					95					

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		336
100							105					110					

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		384
115							120					125					

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		432
130							135					140					

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		480
145							150					155		160			

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc

Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly		528
165							170					175					

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		573	
180							185					190					

<210> 995
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. V163A, S175G mutations

<400> 995

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 996

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. V163A, S175G mutations, and
posit.1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400>	996																
gtg	agc	aag	gac	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc		48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10				15				
gag	ctg	gac	gac	gta	aac	ggc	cac	aag	tgc	agc	gtg	tcc	ggc	gag			96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
20					25					30							
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	tgc	atc	tgc		144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
35					40					45							
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc		192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
50					55					60							
ggc	tac	ggc	ctg	cag	tgc	tgc	tcc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
65					70				75				80				
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc		288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
85					90					95							
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg		336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
100					105					110							
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc		384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
115					120					125							
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
130					135					140							
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc		480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
145					150				155				160				
atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	ggc	gtg		528
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val		
165					170					175							
cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			570	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp				
180					185					190							

<210> 997
 <211> 190
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. V163A, S175G mutations, and
posit.1 Met removed

<400> 997

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 998

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 998
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 999
<211> 191
<212> PRT
<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations

<400> 999

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1000

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 1000

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg 528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1001

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations,
and posit. 1 Met removed

<400> 1001

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1002

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and S175G mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 1002

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gaa ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1003
 <211> 191
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and
 S175G mutations

 <400> 1003

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
 165 170 175

 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 1004
<211> 570
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and S175G mutations, and posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(570)

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1005

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and S175G mutations, and posit. 1 Met removed

<400> 1005

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1006

<211> 147

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(147)

<223> YFP F2F corresponds to aa residues 192-end of YFP

<400> 1006

atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
1 5 10 15

48

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

96

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

144

aag

Lys

147

<210> 1007

<211> 49

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Met added @ position 1

<400> 1007

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

Lys

<210> 1008
 <211> 144
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F2F, with Y203F mutation

 <220>
 <221> CDS
 <222> (1)..(144)

 <400> 1008

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc gcc	48
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala	
1 5 10 15	

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	96
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
20 25 30	

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	144
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
35 40 45	

<210> 1009
 <211> 48
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F2F, with Y203F mutation

 <400> 1009

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala	
1 5 10 15	

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
20 25 30	

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
35 40 45	

<210> 1010
 <211> 147
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F2F, w. Y203F mutation, Met added @ posit. 1

 <220>
 <221> CDS

<222> (1) .. (147)

<400> 1010
atg ggc ccc gtg ctg ccc gac aac cac tac ctg agc ttc cag tcc 48
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
1 5 10 15

gcc ctg agc aaa gac ccc aac gag aag cgcc gat cac atg gtc ctg ctg 96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

aag 147
Lys

<210> 1011
<211> 49
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2F, w. Y203F mutation, Met added @ posit. 1

<400> 1011

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

Lys

<210> 1012
<211> 144
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F2F, with Y203H mutation

<220>
<221> CDS
<222> (1)..(144)

<400> 1012
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc gcc 48
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala
1 5 10 15

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 96
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
20 25 30

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
35 40 45

<210> 1013
 <211> 48
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F2F, with Y203H mutation

 <400> 1013

Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	His	Gln	Ser	Ala
1															15

Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu
															30

Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys
35															45

<210> 1014
 <211> 147
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F2F, w. Y203H mutation, Met added @ posit. 1

 <220>
 <221> CDS
 <222> (1)..(147)

 <400> 1014

atg	ggc	ccc	gtg	ctg	ccc	gac	aac	cac	tac	ctg	agc	cac	cag	tcc	48
Met	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	His	Gln	Ser
1															15

gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	96
Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	
															30	

gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	144
Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	
35															45	

aag															147
Lys															

<210> 1015
 <211> 49
 <212> PRT
 <213> Artificial

 <220>

<223> modif. frag.; YFP F2F, w. Y203H mutation, Met added @ posit. 1

<400> 1015

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

Lys

<210> 1016

<211> 144

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Y203T mutation

<220>

<221> CDS

<222> (1)..(144)

<400> 1016

ggc ccc gtg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 48
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
1 5 10 15

ctg agc aaa gac ccc aac gag aag cgcg gat cac atg gtc ctg ctg gag 96
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
20 25 30

tgc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
35 40 45

<210> 1017

<211> 48

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Y203T mutation

<400> 1017

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
1 5 10 15

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
20 25 30

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
35 40 45

<210> 1018

<211> 147

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, w. Y203T mutation, Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(147)

<400> 1018

atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 48
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
1 5 10 15

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

aag 147
Lys

<210> 1019

<211> 49

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, w. Y203T mutation, Met added @ posit. 1

<400> 1019

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

Lys

<210> 1020
<211> 114
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; RFP F1A, with position 1 Met removed

<220>
<221> CDS
<222> (1)..(114)
<223> RFP F1A corresponds to aa residues 1-39 of mRFP

<400> 1020
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag 114
Glu Gly Arg Pro Tyr Glu
35

<210> 1021
<211> 38
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; RFP F1A, with position 1 Met removed

<400> 1021
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

Glu Gly Arg Pro Tyr Glu
35

<210> 1022
<211> 561
<212> DNA
<213> Artificial

<220>

<223> modif. frag.; RFP F2A, with Met added @ position 1

<220>

<221> CDS

<222> (1) .. (561)

<223> RFP F2A corresponds to aa residues 40-end of mRFP

<400> 1022

```

atg ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg
Met Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu
   1           5           10          15

```

48

```

ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys
          20           25           30

```

96

```

gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
            35           40           45

```

144

ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc
 Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
 50 55 60

192

ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc
Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
65 70 75 80

240

atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc
 Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
 85 90 95

288

```

gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
          100           105           110

```

336

tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
115 120 125

384

```

ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc acc tac atg
Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
    130           135           140

```

432

```

gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
145           150           155           160

```

480

ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac
 Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
 165 170 175

528

```

gag cgc gcc gag ggc cgc cac tcc acc ggc gcc
Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
          180           185

```

561

<210> 1023

<211> 187

<212> PRT
<213> Artificial

<220>
<223> modif. frag.; RFP F2A, with Met added @ position 1

<400> 1023

Met Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu
1 5 10 15

Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys
20 25 30

Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
35 40 45

Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
50 55 60

Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
65 70 75 80

Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
85 90 95

Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
100 105 110

Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
115 120 125

Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
130 135 140

Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
145 150 155 160

Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
165 170 175

Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
180 185

<210> 1024
<211> 300
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; RFP F1B, with position 1 Met removed

<220>
<221> CDS
<222> (1)..(300)
<223> RFP F1B corresponds to aa residues 1-100 of mRFP

<400> 1024

gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac 240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg 288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

aac ttc gag gac 300
Asn Phe Glu Asp
100

<210> 1025

<211> 100

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F1B, with position 1 Met removed

<400> 1025

Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg 15
1 5 10 15

Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

Asn Phe Glu Asp
100

<210> 1026

<211> 375

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2B, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(375)

<223> RFP F2B corresponds to aa residues 102-225(end) of mRFP

<400> 1026

atg ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc 48
Met Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
1 5 10 15

gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac 96
Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
20 25 30

ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag 144
Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
35 40 45

cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg 192
Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
50 55 60

ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc 240
Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
65 70 75 80

tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac 288
Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
85 90 95

atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa 336
Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
100 105 110

cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc
Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
115 120 125

375

<210> 1027

<211> 125

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2B, with Met added @ position 1

<400> 1027

Met Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
1 5 10 15

Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
20 25 30

Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
35 40 45

Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
50 55 60

Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
65 70 75 80

Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
85 90 95

Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
100 105 110

Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
115 120 125

<210> 1028

<211> 342

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F1C, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(342)

<223> RFP F1C corresponds to aa residues 1-115 of mRFP

<400> 1028				
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc				48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg				
1	5	10	15	
atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc				96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly				
20	25	30		
gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc				144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Leu Lys Lys Val Thr				
35	40	45		
aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc				192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe				
50	55	60		
cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac				240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp				
65	70	75	80	
tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg				288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met				
85	90	95		
aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg				336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu				
100	105	110		
cag gac				342
Gln Asp				

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110

Gln Asp

<210> 1030

<211> 333

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2C, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(333)

<223> RFP F2C corresponds to aa residues 116-225(end) of mRFP

<400> 1030

atg ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc
Met Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro
1 5 10 15

48

tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc
Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser
20 25 30

96

acc gag cggtatq tac ccc gag gac ggc gcc ctg aag ggc gag atc aag
Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys
35 40 45

144

atg agg ctg aag gac ggc ggc cac tac gac gcc gag gtc aag
Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys
50 55 60

192

acc acc tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag
Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys
65 70 75 80

240

acc gac atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc
Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile
85 90 95

288

gtg gaa cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc
Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
100 105 110

333

<210> 1031

<211> 111

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2C, with Met added @ position 1

<400> 1031

Met Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro
1 5 10 15

Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser
20 25 30

Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys
35 40 45

Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys
50 55 60

Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys
65 70 75 80

Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile
85 90 95

Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
100 105 110

<210> 1032

<211> 456

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F1D, with position 1 Met removed

<220>

<221> CDS

<222> (1)...(456)

<223> RFP F1D corresponds to aa residues 1-153 of mRFP

<400> 1032

gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15 48

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30 96

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45 144

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
192

50	55	60	
cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp	65	70	240
		75	80
tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met	85	90	288
		95	
aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu	100	105	336
		110	
cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe	115	120	384
		125	
ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala	130	135	432
		140	
tcc acc gag cgg atg tac ccc gag Ser Thr Glu Arg Met Tyr Pro Glu	145	150	456
<210> 1033			
<211> 152			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; RFP F1D, with position 1 Met removed			
<400> 1033			
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg	1	5	10
			15
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly	20	25	30
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr	35	40	45
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe	50	55	60
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp	65	70	75
			80
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met	85	90	95

Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110

Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
115 120 125

Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
130 135 140

Ser Thr Glu Arg Met Tyr Pro Glu
145 150

<210> 1034

<211> 219

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2D, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(219)

<223> RFP F2D corresponds to aa residues 154-225(end) of mRFP

<400> 1034

atg gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag ctg aag 48
Met Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys Leu Lys
1 5 10 15

gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag 96
Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
20 25 30

aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac 144
Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
35 40 45

atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc 192
Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
50 55 60

gcc gag ggc cgc cac tcc acc ggc gcc 219
Ala Glu Gly Arg His Ser Thr Gly Ala
65 70

<210> 1035

<211> 73

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2D, with Met added @ position 1

<400> 1035

1006

Met Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys Leu Lys
1 5 10 15

Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
20 25 30

Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
35 40 45

Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
50 55 60

Ala Glu Gly Arg His Ser Thr Gly Ala
65 70

<210> 1036

<211> 504

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F1E, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(504)

<223> RFP F1E corresponds to aa residues 1-169 of mRFP

<400> 1036
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac 240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg 288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg		336	
Asn Phe Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu			
100	105	110	
cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc		384	
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe			
115	120	125	
ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc		432	
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala			
130	135	140	
tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc		480	
Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile			
145	150	155	160
aag atg agg ctg aag ctg aag gac		504	
Lys Met Arg Leu Lys Leu Lys Asp			
165			

<210> 1037

<211> 168

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F1E, with position 1 Met removed

<400> 1037

Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg			
1	5	10	15

Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly		
20	25	30

Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr		
35	40	45

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe		
50	55	60

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp			
65	70	75	80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met		
85	90	95

Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu		
100	105	110

Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
115 120 125

Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
130 135 140

Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile
145 150 155 160

Lys Met Arg Leu Lys Leu Lys Asp
165

<210> 1038

<211> 171

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2E, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(171)

<223> RFP F2E corresponds to aa residues 170-225(end) of mRFP

<400> 1038

atg ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag 48
Met Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
1 5 10 15

aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac 96
Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
20 25 30

atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc 144
Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
35 40 45

gcc gag ggc cgc cac tcc acc ggc gcc 171
Ala Glu Gly Arg His Ser Thr Gly Ala
50 55

<210> 1039

<211> 57

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2E, with Met added @ position 1

<400> 1039

Met Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys

1 5 10 15
Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
20 25 30

Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
35 40 45

Ala Glu Gly Arg His Ser Thr Gly Ala
50 55

<210> 1040

<211> 549

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F1F, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(549)

<223> RFP F1F corresponds to aa residues 1-184 of mRFP

<400> 1040

gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
Lys Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac 240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg 288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

aac ttc gag gac ggc ggc gtg acc gtg acc cag gac tcc tcc ctg 336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110

cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc 384
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe

115	120	125	
ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala 130	135	140	432
tcc acc gag cg ^g atg tac ccc gag gac ggc gcc ctg aag ggc gag atc Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile 145	150	155	480
aag atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val 165	170	175	528
aag acc acc tac atg gcc aag Lys Thr Thr Tyr Met Ala Lys 180			549
<210> 1041			
<211> 183			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; RFP F1F, with position 1 Met removed			
<400> 1041			
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg 1 5 10 15			
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly 20 25 30			
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr 35 40 45			
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe 50 55 60			
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp 65 70 75 80			
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met 85 90 95			
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu 100 105 110			
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe 115 120 125			

Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
130 135 140

Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile
145 150 155 160

Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val
165 170 175

Lys Thr Thr Tyr Met Ala Lys
180

<210> 1042

<211> 126

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2F, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(126)

<223> RFP F2F corresponds to aa residues 185-225(end) of mRFP

<400> 1042

atg aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg 48
Met Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu
1 5 10 15

gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag 96
Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu
20 25 30

cgc gcc gag ggc cgc cac tcc acc ggc gcc 126
Arg Ala Glu Gly Arg His Ser Thr Gly Ala
35 40

<210> 1043

<211> 42

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2F, with Met added @ position 1

<400> 1043

Met Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu
1 5 10 15

Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu

20

25

30

Arg Ala Glu Gly Arg His Ser Thr Gly Ala
35 40

<210> 1044

<211> 105

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1A, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(105)

<223> KFP F1A corresponds to aa residues 1-36 of KFP1

<400> 1044

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

48

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

96

ccc ttc gag

Pro Phe Glu

35

105

<210> 1045

<211> 35

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F1A, with position 1 Met removed

<400> 1045

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

Pro Phe Glu

35

<210> 1046

<211> 591

<212> DNA

<213> Artificial

<220>
<223> modif. frag.; KFP F2A, with Met added @ position 1

<220>
<221> CDS
<222> (1)..(591)
<223> KFP F2A corresponds to aa residues 37-end of KFP1

<400> 1046		
atg ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc ccc ctg		48
Met Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly Pro Leu		
1 5 10 15		
ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc tcc aag		96
Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly Ser Lys		
20 25 30		
acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag cag tcc		144
Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys Gln Ser		
35 40 45		
ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag gac ggc		192
Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr Glu Asp Gly		
50 55 60		
ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac tgc ctg		240
Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp Cys Leu		
65 70 75 80		
gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac ggc ccc		288
Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp Gly Pro		
85 90 95		
gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag atc gtg		336
Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu Ile Val		
100 105 110		
tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc ctg aag		384
Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala Leu Lys		
115 120 125		
tgc ccc ggc ggc cg ^g cac ctg acc tgc cac ctg cac acc acc tac cgc		432
Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr Tyr Arg		
130 135 140		
tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac ttc gag		480
Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu		
145 150 155 160		
gac cac cgc atc gag atc atg gag gag gtg gag aag ggc aag tgc tac		528
Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr		
165 170 175		
aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc		576
Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser		
180 185 190		
aag ctg ggc cac aac		591
Lys Leu Gly His Asn		

<210> 1047

<211> 197

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F2A, with Met added @ position 1

<400> 1047

Met	Gly	Thr	Gln	Glu	Met	Lys	Ile	Glu	Val	Ile	Glu	Gly	Gly	Pro	Leu
1					5				10					15	

Pro	Phe	Ala	Phe	His	Ile	Leu	Ser	Thr	Ser	Cys	Met	Tyr	Gly	Ser	Lys
					20			25					30		

Thr	Phe	Ile	Lys	Tyr	Val	Ser	Gly	Ile	Pro	Asp	Tyr	Phe	Lys	Gln	Ser
					35			40					45		

Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Tyr	Glu	Asp	Gly
					50		55				60			

Gly	Phe	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Asp	Gly	Asp	Cys	Leu
					65		70			75			80		

Val	Tyr	Lys	Val	Lys	Ile	Leu	Gly	Asn	Asn	Phe	Pro	Ala	Asp	Gly	Pro
					85			90					95		

Val	Met	Gln	Asn	Lys	Val	Gly	Arg	Trp	Glu	Pro	Gly	Thr	Glu	Ile	Val
					100			105					110		

Tyr	Glu	Val	Asp	Gly	Val	Leu	Arg	Gly	Gln	Ser	Leu	Met	Ala	Leu	Lys
					115			120			125				

Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr	Thr	Tyr	Arg
					130			135			140				

Ser	Lys	Lys	Pro	Ala	Ser	Ala	Leu	Lys	Met	Pro	Gly	Phe	His	Phe	Glu
							145		150		155		160		

Asp	His	Arg	Ile	Glu	Ile	Met	Glu	Glu	Val	Glu	Lys	Gly	Lys	Cys	Tyr
					165				170				175		

Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala	Ala	Pro	Ser
						180			185			190			

Lys Leu Gly His Asn
195

<210> 1048

<211> 291

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1B, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(291)

<223> KFP F1B corresponds to aa residues 1-98 of KFP1

<400> 1048

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc 48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac 96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc 144
Pro Phe Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc 192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag 240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc tac gag 288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr Glu
85 90 95

gac

Asp

291

<210> 1049

<211> 97

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F1B, with position 1 Met removed

<400> 1049

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly

1

5

10

15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85 90 95

Asp

<210> 1050

<211> 405

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2B, with Met added @ position 1

<220>

<221> CDS

<222> (1)...(405)

<223> KFP F2B corresponds to aa residues 99-end of KFP1

<400> 1050

atg ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac
Met Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
1 5 10 15

48

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
20 25 30

96

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
35 40 45

144

atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
50 55 60

192

ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc
Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
65 70 75 80

240

tac	cgc	tcc	aag	aag	ccc	gcc	tcc	gcc	ctg	aag	atg	ccc	ggc	ttc	cac		288
Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ser	Ala	Leu	Lys	Met	Pro	Gly	Phe	His		
85									90						95		
ttc	gag	gac	cac	cgc	atc	gag	atc	atg	gag	gag	gtg	gag	aag	ggc	aag		336
Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Met	Glu	Glu	Val	Glu	Lys	Gly	Lys		
100								105						110			
tgc	tac	aag	cag	tac	gag	gcc	gcc	gtg	ggc	cgc	tac	tgc	gac	gcc	gcc		384
Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala	Ala		
115								120				125					
ccc	tcc	aag	ctg	ggc	cac	aac											405
Pro	Ser	Lys	Leu	Gly	His	Asn											
130						135											
<210>	1051																
<211>	135																
<212>	PRT																
<213>	Artificial																
<220>																	
<223>	modif. frag. ; KFP F2B, with Met added @ position 1																
<400>	1051																
Met	Gly	Gly	Phe	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Asp	Gly	Asp		
1				5					10					15			
Cys	Leu	Val	Tyr	Lys	Val	Lys	Ile	Leu	Gly	Asn	Asn	Phe	Pro	Ala	Asp		
				20				25						30			
Gly	Pro	Val	Met	Gln	Asn	Lys	Val	Gly	Arg	Trp	Glu	Pro	Gly	Thr	Glu		
				35				40						45			
Ile	Val	Tyr	Glu	Val	Asp	Gly	Val	Leu	Arg	Gly	Gln	Ser	Leu	Met	Ala		
				50				55						60			
Leu	Lys	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr	Thr		
				65				70			75			80			
Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ser	Ala	Leu	Lys	Met	Pro	Gly	Phe	His		
				85				90						95			
Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Met	Glu	Glu	Val	Glu	Lys	Gly	Lys		
				100				105						110			
Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala	Ala		
				115				120				125					

Pro Ser Lys Leu Gly His Asn
130 135

<210> 1052

<211> 456

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1C, with position 1 Met removed

<220>

<221> CDS

<222> (1)...(456)

<223> KFP F1C corresponds to aa residues 1-153 of KFP1

<400> 1052

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

48

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

96

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

144

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

192

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

240

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr Glu
85 90 95

288

gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100 105 110

336

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115 120 125

384

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
130 135 140

432

atc gtg tac gag gtg gac ggc gtg
Ile Val Tyr Glu Val Asp Gly Val
145 150

456

<210> 1053
<211> 152
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; KFP F1C, with position 1 Met removed

<400> 1053

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr Glu
85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100 105 110

Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115 120 125

Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
130 135 140

Ile Val Tyr Glu Val Asp Gly Val
145 150

<210> 1054
<211> 240
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; KFP F2C, with Met added @ position 1

<220>

<221> CDS
<222> (1)..(240)
<223> KFP F2C corresponds to aa residues 154-end of KFP1

<400> 1054
atg ctg cgc ggc cag tcc ctg atg gcc ctg aag tgc ccc ggc ggc cg... 48
Met Leu Arg Gly Gln Ser Leu Met Ala Leu Lys Cys Pro Gly Gly Arg
1 5 10 15

cac ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc 96
His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
20 25 30

tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag 144
Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu
35 40 45

atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc 192
Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala
50 55 60

gcc gtg ggc cgc tac tgc gac gcc ccc tcc aag ctg ggc cac aac 240
Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
65 70 75 80

<210> 1055
<211> 80
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; KFP F2C, with Met added @ position 1

<400> 1055

Met Leu Arg Gly Gln Ser Leu Met Ala Leu Lys Cys Pro Gly Gly Arg
1 5 10 15

His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
20 25 30

Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu
35 40 45

Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala
50 55 60

Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
65 70 75 80

<210> 1056
<211> 333
<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1D, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(333)

<223> KFP F1D corresponds to aa residues 1-112 of KFP1

<400> 1056

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

48

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc qag ggc aac
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

96

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

144

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

192

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

240

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr Glu
85 90 95

288

gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
100 105 110

333

<210> 1057

<211> 111

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F1D, with position 1 Met removed

<400> 1057

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly

35

40

45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
100 105 110

<210> 1058

<211> 363

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2D, with Met added @ position 1

<220>

<221> CDS

<222> (1)...(363)

<223> KFP F2D corresponds to aa residues 113-end of KFP1

<400> 1058

atg gac tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc
Met Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro
1 5 10 15

48

gcc gac ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga
Ala Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly
20 25 30

96

acc gag atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg
Thr Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu
35 40 45

144

atg gcc ctg aag tgc ccc ggc ggc cac ctg acc tgc cac ctg cac
Met Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His
50 55 60

192

acc acc tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc
Thr Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly
65 70 75 80

240

ttc cac ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag
Phe His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys
85 90 95

288

ggc aag tgc tac aag cag tac gag gcc gtc ggc cgc tac tgc gac
Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp
100 105 110

336

gcc gcc ccc tcc aag ctg ggc cac aac
Ala Ala Pro Ser Lys Leu Gly His Asn
115 120

363

<210> 1059

<211> 121

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F2D, with Met added @ position 1

<400> 1059

Met Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro
1 5 10 15

Ala Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly
20 25 30

Thr Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu
35 40 45

Met Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His
50 55 60

Thr Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly
65 70 75 80

Phe His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys
85 90 95

Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp
100 105 110

Ala Ala Pro Ser Lys Leu Gly His Asn
115 120

<210> 1060

<211> 504

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1E, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(504)

<223> KFP F1E corresponds to aa residues 1-169 of KFP1

<400> 1060
 gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc 48
 Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
 1 5 10 15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac 96
 Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
 20 25 30

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc 144
 Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
 35 40 45

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc 192
 Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
 50 55 60

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag 240
 Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
 65 70 75 80

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag 288
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95

gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac 336
 Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
 100 105 110

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac 384
 Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
 115 120 125

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag 432
 Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
 130 135 140

atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc 480
 Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
 145 150 155 160

ctg aag tgc ccc ggc ggc cgg cac 504
 Leu Lys Cys Pro Gly Gly Arg His
 165

<210> 1061

<211> 168

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F1E, with position 1 Met removed

<400> 1061

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100 105 110

Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115 120 125

Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
130 135 140

Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145 150 155 160

Leu Lys Cys Pro Gly Gly Arg His
165

<210> 1062

<211> 192

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2E, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(192)

<223> KFP F2E corresponds to aa residues 170-end of KFP1

<400> 1062

atg ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc
Met Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
1 5 10 15

48

tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag	96
Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu	
20 25 30	
atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc	144
Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala	
35 40 45	
gcc gtg ggc cgc tac tgc gac gcc ccc tcc aag ctg ggc cac aac	192
Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn	
50 55 60	
<210> 1063	
<211> 64	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; KFP F2E, with Met added @ position 1	
<400> 1063	
Met Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala	
1 5 10 15	
Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu	
20 25 30	
Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala	
35 40 45	
Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn	
50 55 60	
<210> 1064	
<211> 555	
<212> DNA	
<213> Artificial	
<220>	
<223> modif. frag.; KFP F1F, with position 1 Met removed	
<220>	
<221> CDS	
<222> (1)..(555)	
<223> KFP F1F corresponds to aa residues 1-186 of KFP1	
<400> 1064	
gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc	48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
1 5 10 15	

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac	96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn	
20 25 30	
ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc	144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly	
35 40 45	
ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc	192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly	
50 55 60	
tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag	240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys	
65 70 75 80	
cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag	288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr Glu	
85 90 95	
gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac	336
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp	
100 105 110	
tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac	384
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp	
115 120 125	
ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag	432
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu	
130 135 140	
atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc	480
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala	
145 150 155 160	
ctg aag tgc ccc ggc ggc cg ^g cac ctg acc tgc cac ctg cac acc acc	528
Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr	
165 170 175	
tac cgc tcc aag aag ccc gcc tcc gcc	555
Tyr Arg Ser Lys Lys Pro Ala Ser Ala	
180 185	
<210> 1065	
<211> 185	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; KFP F1F, with position 1 Met removed	
<400> 1065	
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
1 5 10 15	

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100 105 110

Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115 120 125

Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
130 135 140

Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145 150 155 160

Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
165 170 175

Tyr Arg Ser Lys Lys Pro Ala Ser Ala
180 185

<210> 1066

<211> 141

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2F, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(141)

<223> KFP F2F corresponds to aa residues 187-end of KFP1

<400> 1066
 atg ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag atc 48
 Met Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu Ile
 1 5 10 15

 atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc gcc 96
 Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala
 20 25 30

 gtg ggc cgc tac tgc gac gcc ccc tcc aag ctg ggc cac aac 141
 Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
 35 40 45

<210> 1067
 <211> 47
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; KFP F2F, with Met added @ position 1

<400> 1067

 Met Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu Ile
 1 5 10 15

Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala
 20 25 30

Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
 35 40 45